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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=11; day=7; hr=14; min=34; sec=38; ms=420;]

=====

Reviewer Comments:

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120

attagggcatg gggccgaagt tcatgcagtg atgagtgagg cagccaccaa gataattcat
180

The above lines are a sample of "wrapped" nucleotide totals appearing under their respective lines. Please do not open and save a PatentIn-generated file in a word processing software; PatentIn margins are fixed, and re-saving the file in a word processing program will "skew" the margins. Same error in Sequences 20-36, and throughout the file.

Application No: 09631613 Version No: 3.0

Input Set:

Output Set:

Started: 2008-10-07 15:07:33.186
Finished: 2008-10-07 15:07:53.432
Elapsed: 0 hr(s) 0 min(s) 20 sec(s) 246 ms
Total Warnings: 83
Total Errors: 401
No. of SeqIDs Defined: 89
Actual SeqID Count: 89

| Error code | Error Description |
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| W 213 | Artificial or Unknown found in <213> in SEQ ID (1) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (2) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (3) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (4) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (5) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (6) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (7) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (8) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (9) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (10) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (11) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (12) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (13) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (14) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (15) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (16) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (17) |
| E 254 | The total number of bases conflicts with running total Input: 0, Calculated : 60 SEQID(18) |
| E 323 | Invalid/missing amino acid numbering SEQID (18) POS (2) |

Input Set:

Output Set:

Started: 2008-10-07 15:07:33.186
Finished: 2008-10-07 15:07:53.432
Elapsed: 0 hr(s) 0 min(s) 20 sec(s) 246 ms
Total Warnings: 83
Total Errors: 401
No. of SeqIDs Defined: 89
Actual SeqID Count: 89

| Error code | Error Description |
|------------|---|
| E 323 | Invalid/missing amino acid numbering SEQID (18)at Protein (5) |
| E 323 | Invalid/missing amino acid numbering SEQID (18)at Protein (10) |
| E 323 | Invalid/missing amino acid numbering SEQID (18)at Protein (15) |
| E 254 | The total number of bases conflicts with running total Input: 0, Calculated : 120 SEQID(18) |
| E 323 | Invalid/missing amino acid numbering SEQID (18) POS (1) |
| E 323 | Invalid/missing amino acid numbering SEQID (18) POS (2) |
| E 323 | Invalid/missing amino acid numbering SEQID (18)at Protein (5) |
| E 323 | Invalid/missing amino acid numbering SEQID (18)at Protein (10) |
| E 323 | Invalid/missing amino acid numbering SEQID (18)at Protein (15) |
| E 254 | The total number of bases conflicts with running total Input: 0, Calculated : 180 SEQID(18) |
| E 323 | Invalid/missing amino acid numbering SEQID (18) POS (1) |
| E 323 | Invalid/missing amino acid numbering SEQID (18) POS (2) |
| E 323 | Invalid/missing amino acid numbering SEQID (18)at Protein (5) |
| E 323 | Invalid/missing amino acid numbering SEQID (18)at Protein (10) |
| E 323 | Invalid/missing amino acid numbering SEQID (18)at Protein (15) |
| E 254 | The total number of bases conflicts with running total Input: 0, Calculated : 240 SEQID(18) |
| E 323 | Invalid/missing amino acid numbering SEQID (18) POS (1) |
| E 323 | Invalid/missing amino acid numbering SEQID (18) POS (2) |
| E 323 | Invalid/missing amino acid numbering SEQID (18)at Protein (5) |
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Input Set:

Output Set:

Started: 2008-10-07 15:07:33.186
Finished: 2008-10-07 15:07:53.432
Elapsed: 0 hr(s) 0 min(s) 20 sec(s) 246 ms
Total Warnings: 83
Total Errors: 401
No. of SeqIDs Defined: 89
Actual SeqID Count: 89

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| E 254 | The total number of bases conflicts with running total Input: 0, Calculated : 420 SEQID(18) |
| E 254 | The total number of bases conflicts with running total Input: 0, Calculated : 480 SEQID(18) |
| E 254 | The total number of bases conflicts with running total Input: 0, Calculated : 540 SEQID(18) |
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| E 254 | The total number of bases conflicts with running total Input: 0, Calculated : 900 SEQID(18) |
| E 254 | The total number of bases conflicts with running total Input: 0, Calculated : 960 SEQID(18) |
| E 254 | The total number of bases conflicts with running total Input: 0, Calculated : 1020 SEQID(18) |
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Input Set:

Output Set:

Started: 2008-10-07 15:07:33.186
Finished: 2008-10-07 15:07:53.432
Elapsed: 0 hr(s) 0 min(s) 20 sec(s) 246 ms
Total Warnings: 83
Total Errors: 401
No. of SeqIDs Defined: 89
Actual SeqID Count: 89

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| W 402 | Undefined organism found in <213> in SEQ ID (47) |

SEQUENCE LISTING

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Hansen, Connie J

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Complexes, Isolated PEF Proteins, and Methods for
Purifying and Identifying Them

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<140> 09631613

<141> 2000-08-04

<150> US 08/957,709

<151> 1997-10-24

<150> US 08/822,774

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1 5 10 15

Xaa Xaa

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| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

Ile Glu

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| | gccatdatna cdgertcgta ttt | 23 |
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| | ardacdacyt grttttcttc | 20 |
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120

attaggcatg gggccgaagt tcatgcagtg atgagtgagg cagccacca gataattcat
180

ccttatgcat ggaatttgcc cacgggaaat ccagtcataa ctgagatcac tggatttato
240

gagcatgttg agttagcagg ggaacatgag aataaagcag atttaatttt ggtttgcct
300

gccactgcc aacaaattag taagattgca tgtggaatag atgatactcc agtaactaca
360

gtcgtgacca cagcatttcc ccacattcca attatgatag cccagcaat gcatgagaca
420

atgtacaggc atcccatagt aaggggagaac attgaaaggt taaagaagct tggcgttgag
480

tttataggac caagaattga ggaggggaaag gcaaaaagttg caagcattga tgaaatagtt
540

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600

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840

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900

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960

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35 40 45

Ala Val Met Ser Glu Ala Ala Thr Lys Ile Ile His Pro Tyr Ala Trp
50 55 60

Asn Leu Pro Thr Gly Asn Pro Val Ile Thr Glu Ile Thr Gly Phe Ile
65 70 75 80

Glu His Val Glu Leu Ala Gly Glu His Glu Asn Lys Ala Asp Leu Ile
85 90 95

Leu Val Cys Pro Ala Thr Ala Asn Thr Ile Ser Lys Ile Ala Cys Gly
100 105 110

Ile Asp Asp Thr Pro Val Thr Thr Val Val Thr Thr Ala Phe Pro His
115 120 125

Ile Pro Ile Met Ile Ala Pro Ala Met His Glu Thr Met Tyr Arg His
130 135 140

Pro Ile Val Arg Glu Asn Ile Glu Arg Leu Lys Lys Leu Gly Val Glu
145 150 155 160

Phe Ile Gly Pro Arg Ile Glu Glu Gly Arg Ala Lys Val Ala Ser Ile
165 170 175

Asp Glu Ile Val Tyr Arg Val Ile Lys Lys Leu His Lys Lys Thr Leu
180 185 190

Glu Gly Lys Arg Val Leu Val Thr Ala Gly Ala Thr Arg Glu Tyr Ile
195 200 205

Asp Pro Ile Arg Phe Ile Thr Asn Ala Ser Ser Gly Lys Met Gly Val
210 215 220

Ala Leu Ala Glu Glu Ala Asp Phe Arg Gly Ala Val Thr Leu Ile Arg
225 230 235 240

Thr Lys Gly Ser Val Lys Ala Phe Arg Ile Arg Lys Ile Lys Leu Lys
245 250 255

Val Glu Thr Val Glu Glu Met Leu Ser Ala Ile Glu Asn Glu Leu Arg
260 265 270

Ser Lys Lys Tyr Asp Val Val Ile Met Ala Ala Ala Val Ser Asp Phe
275 280 285

Arg Pro Lys Ile Lys Ala Glu Gly Lys Ile Lys Ser Gly Arg Ser Ile
290 300

Thr Ile Glu Leu Val Pro Xaa Asn Pro Lys Ile Ile Asp Arg Ile Lys

305 310 315 320

Glu Ile Gln Pro Asn Val Phe Leu Val Gly Phe Lys Ala Glu Thr Ser
325 330 335

Lys Glu Lys Leu Ile Glu Glu Gly Lys Arg Gln Ile Glu Arg Ala Lys
340 345 350

Ala Asp Leu Val Val Gly Asn Thr Leu Glu Ala Phe Gly Ser Glu Glu
355 360 365

Asn Gln Val Val Leu Ile Gly Arg Asp Phe Thr Lys Glu Leu Pro Lys
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23

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gagttaaatg cctacactgt atct

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<400> 37

Glu Trp Ala Glu Arg Leu Leu Leu Arg Gly Asn Xaa Ser Lys Trp Lys
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Arg Lys Glu Lys Ser Xaa Phe Leu Gln Gly Asn
20 25

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